WHAT IS CLAIMED IS

~~Patent Claims~~

1. An isolated polynucleotide containing a polynucleotide sequence selected from the group

a) polynucleotide which is at least 70% identical to a polynucleotide which codes for a polypeptide containing the amino acid sequence of SEQ ID no. 2,

b) polynucleotide which codes for a polypeptide which contains an amino acid sequence which is at least 70% identical to the amino acid sequence of SEQ ID no. 2,

c) polynucleotide which is complementary to the polynucleotides of a) or b) and

d) polynucleotide containing at least 15 successive bases of the polynucleotide sequence of a), b) or c).

2. The polynucleotide as claimed in claim 1, wherein the polynucleotide is a replicable, preferably recombinant DNA.

3. The polynucleotide as claimed in claim 1, wherein the polynucleotide is an RNA.

4. The polynucleotide as claimed in claim 2, containing the nucleic acid sequence as shown in SEQ ID no. 1.

5. The polynucleotide sequence as claimed in claim 2, which codes for a polypeptide which contains the amino acid sequence shown in SEQ ID no. 2.

6. The replicable DNA as claimed in claim 2, containing

(i) the nucleotide sequence shown in SEQ ID no. 1, or

(ii) at least one sequence which matches the sequence (i) within the degeneration range of the genetic code, or

(iii) at least one sequence which hybridises with the complementary sequence to sequence (i) or (ii) and optionally

(iv) functionally neutral sense mutations in (i).

7. A vector containing the polynucleotide as claimed in claim 1, in particular point d, deposited in E. coli DSM 13114.

8. Coryneform bacteria acting as host cell which contain a deletion or an insertion in the poxB gene.

9. A process for the production of amino acids, in particular L-lysine,
w h e r e i n
the following steps are performed:

a) fermentation of the bacteria producing the desired L-amino acid bacteria, in which at least the poxB gene is attenuated,

b) accumulation of the desired L-amino acid in the medium or in the cells of the bacteria and

c) isolation of the L-amino acid.

10. The process as claimed in claim 9,
w h e r e i n
bacteria are used in which further genes of the

biosynthetic pathway of the desired L-amino acid are additionally amplified.

11. The process as claimed in claim 9, wherein bacteria are used in which the metabolic pathways which reduce the formation of the desired L-amino acid are at least partially suppressed.

12. The process as claimed in claim 9, wherein expression of the polynucleotide as claimed in claim 1, in particular 1a to 1c, is reduced.

13. The process as claimed in claim 9, wherein the catalytic properties of the polypeptide (enzyme protein), for which the polynucleotide as claimed in claim 1, in particular 1a to 1c, codes, are reduced.

14. The process as claimed in claim 9, wherein bacteria are used in which attenuation is achieved by using integration mutagenesis by means of the plasmid pCR2.1poxBint, shown in Figure 1 and deposited as DSM 13114, or one of the constituents thereof.

15. The process as claimed in claim 9, wherein L-lysine is produced by fermenting bacteria in which one or more genes are simultaneously over-expressed which are selected from the group

- the dapA gene which codes for dihydropicolinate synthase,
- the DNA fragment which imparts S-(2-aminoethyl)-cysteine resistance,

- the pyc gene which codes for pyruvate carboxylase,
- the dapE gene which codes for succinyldiamino-pimelate desuccinylase,
- the dap gene which codes for glyceraldehyde 3-phosphate dehydrogenase,
- the mqo gene which codes for malate:quinone oxidoreductase
- the lysE gene which codes for lysine export.

16. Process as claimed in one or more of the preceding claims,
w h e r e i n
microorganisms of the genus Corynebacterium glutamicum are used.

add B2